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Research Article

Study on gene action and combining ability for yield and its attributes in upland rice lines of Himachal Pradesh

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Abstract

The present study was conducted to estimate gene action and combining abilityof 12 ricelines bred for upland conditions and 3 testers along with 36 cross combinations developed through line x tester mating design in *Kharif* 2019 and 2020. The crossing was done in *Kharif* 2019 and the material developed was grown and evaluated along with its parentsin randomized block design in *Kharif* 2020. Statistical analysis of the observed data for 14 yield and yield related traits revealed that the dominance variance was higher than the additive variance for all the traits studied except total tillers per plant, grain breadth and L: B ratio. Moreover, the average degree of dominance was greater than 1 for most of the traits, indicating the preponderance of non- additive gene action in governance of these traits and the scope of exploitation of non- additive gene action for further improvement.Significant GCA and SCA effects were found for the lines and crosses, respectively. The lines showing significant GCA effects were HPR 2884, HPR 2871, HPR 2873, and HPR 2889, while the crosses HPR 2866 x HPR 2656, HPR 2866 x HPR 1156, and HPR 2840 x HPR 1156 showed high SCA for various traits.

Key words: Gene action, general combining ability, specific combining ability, variance

1. Introduction

Rice is a staple food crop that is grown throughout many places around the globe. Rice cultivation covers 160.6 million hectares worldwide, with a production of 492.2 million tonnes (Anonymous, 2019a), with India accounting for 42.2 million hectares and 104 million tonnes, bringing it first in the world's total cereal production (Anonymous, 2019b). In hilly regions like Himachal Pradesh and Uttarakhand, it is also a staple food crop. It is grown over an estimated 77 thousand ha. in H.P., with yield of 131.6 thousand tonnes and productivity of 17.05 quintals per hectare (Anonymous, 2019c), with upland rice accounting for 42% of total rice cultivation area.

Lowland transplanted rice requires huge amount of labour and water for puddling as well as in later stages of cultivation. Due to less availability of labour and unpredictable rainfall in hilly areas, it is very difficult to grow transplanted rice. Also, due to undulated topography, the retention of water in rice fields is difficult. As a result, major rice cultivation in hilly areas is done in upland and rainfed conditions. Hence, developing high yielding cultivars suitable for upland and rainfed conditions is necessary for direct sowing.Furthermore, because the area under cultivation is shrinking due to urbanisation and industrialization, a large increase in rice yield potential is required to maintain food security for an exponentially growing population. To secure future food security, we must encourage the breeding and cultivation of single cross rice hybrids (Rasheed *et al.,* 2021). The studies on gene action are necessary for the selection of parents for various hybridization programs and for the choice of suitable breeding procedure for genetic improvement of various quantitative traits. The genetic variances as well as the combining ability effects are used as the measures of gene action. Good general combing ability parents can be selected by combining ability analysis and can be used in hybridization programme to obtain suitable segregants in further generations. High GCA is the result of additive gene action between the hybridizing parents. It has already been exploited in several countries to develop high yielding rice varieties. High SCA is the result of dominance and epistasis effects existing between the hybridizing parents. It is the average performance of a specific cross combination from the population mean. Also, if two parents carry different genes for traits in question, they will tend to complement each other for making good genetic constitution. The non-additive gene action remains unutilized. Both types of gene actions appear to play a considerable role in rice.The breeders often face the problem of selecting parents and crossesto breedfor high yielding crop plants. Hence, there is a constant need to screen germplasm, isolate potential combining lines and desirable cross combinations either to exploit heterosis or to obtain new recombinants. Thus, any method which would help in choosing desirable parents and crosses, would be important for the breeders. Presence of specific combining ability (SCA) effects for yield and yield related traits in rice hybrids are reported by Behera and Monalisa (2016), Morais *et al.* (2017), Faiz *et al.* (2006), Sarker *et al.* (2002) and Kargbo*et al.* (2019). Moreover, studies on gene action are necessary for the selection of parents for various hybridization programs and for the choice of suitable breeding procedure for genetic improvement of various quantitative traits. El Mowafi *et al.*(2021) also emphasised that hybrid rice parental lines with good combining abilities provide an efficient tool for increasing rice production.

2. Materials and Methods

2.1 Materialsused

This investigation was carried out during *Kharif,* 2019 and 2020. The experimental material consisting F_1 population of 36 crosses was developed by crossing 12 lines/genotypes *viz.,* HPR 2643, HPR 2648, HPR 2840, HPR 2843, HPR 2866, HPR 2870, HPR 2871, HPR 2873, HPR 2877, HPR 2884, HPR 2887, HPR 2889 with three testers HPR 1156 (SukaraDhan 1), HPR 2656 (Him Palam Dhan 1) & HPR 2795 (Him Palam Lal Dhan 1)in line × tester mating design at RWRC, Malan, during *Kharif,* 2019. During Kharif 2020, the F_1's of 36 crosses [lines (12) + testers (3)], along with their parents, were evaluated in RBD with three replications in a single row of 2m length, with row to row and plant to plant spacing of 20 cm 15 cm, respectively.

2.2 Observations recorded

In this study, 12 genotypes of rice (lines) suitable for upland conditions were crossed with three testers in line ×tester mating design and the F_1 material along with parents (lines + testers) were evaluated for 14 morphological traits. These traits are days to 50% flowering, days to maturity, plant height (cm), panicle length (cm), total tillers/plant, effective tillers/plant, spikelets/panicle, grains/panicle, spikelet fertility (%), grain yield/plant (g), 1000-grain weight (g), grain length (mm), grain breadth (mm), length: breadth (L: B) ratio. Except for days to 50% flowering and days to maturity, which were recorded on a plot basis, all the other observations were made on five random plants of each genotype/cross combination for various variables. The plants were raised entirely under upland and rainfed conditions without any artificial irrigation.

2.3 Statistical Analysis

The analysis of variance (ANOVA) was done as per Panse and Sukhatme (1985) and combining ability analysis was done following the method of Kempthorne (1957).

3. Results and Discussion

The following results were obtained from the present investigation with respect to ANOVA, gene action and combining ability for all the traits studied which are presented in this section.

The analysis of variance (Table 1) showed that among all the traits under study, except grain breadth, all the other traits were significant. L:B ratio, 1000-grain weight and total tillers per plant were significant only at 5% and rest others were significant at both 5% and 1% level of significance.

The estimation of additive and dominance components of variance was done and the results have been shown in Table 2. Except for total tillers per plant and grain yield per plant, where additive variance was substantially greater, dominance variance was much higher than additive variance for other characters.

Table 1. Analysis of variance of RBD with respect to total entries for all the traits studied

V		**Mean sum of square**	
Sources of variation	**Replication**	**Entries**	**Error**
Degree of freedom	**2**	**50**	**100**
Traits			
Days to maturity	0.18	127.99**	1.04
Days to 50% flowering	5.89	147.70**	1.43
Plant height	56.18	291.67**	58.37
Panicle length	28.49	9.63**	4.24
Total tillers/plant	14.79	3.83*	2.55
Effective tillers/plant	0.52	7.63**	2.06
1000 grain weight	3.88	18.93*	11.05
Grain length	0.12	0.89**	0.16
Grain breadth	0.06	0.04	0.03
L:B ratio	0.51	0.19*	0.12
Spikelets per panicle	2216.56	1489.19**	292.39
Grains per panicle	396.98	1309.12**	110.29
Spikelet fertility	661.72	125.39*	43.03
Grain yield per plant	21.77	111.82*	9.89

*significant at 5% level **significant at 1% level

The average degree of dominance for most of the characters was greater than 1, with the exception of total tillers per plant, indicating that dominant gene action or non-additive gene action predominated in the expression of the majority of characters, revealing their potential for use inexploitation of non-additive gene action for grain yield and other component traits by using genotypes in heterosis breeding and it also shows that the early selection will notbe effective for these genotypes since most of the genotypes will segregate for many characters in future generations.

Table 2. Estimates of additive (and dominance genetic variance (and average degree of dominance)

Traits	**Additive variance**	**Dominance variance**	**Average degree of dominance**
Days to 50% flowering	-1.89	46.03	-
Days to maturity	-1.21	34.38	-
Plant height	13.68	33.79	1.57
Panicle length	0.10	0.44	2.07
Total tillers/plant	0.06	0.06	0.97
Effective tillers/plant	-0.09	0.99	-
Spikelets/panicle	-8.56	348.77	-
Grains/panicle	41.53	235.03	2.37
Spikelet fertility	8.27	13.43	1.27
Grain yield/plant	20.75	13.81	1.50
1000-Grain weight	0.78	1.74	1.49
Grain length	0.001	0.15	10.28
Grain breadth	0.002	0.002	1
L:B ratio	-0.002	0.005	-

For the variables plant height, number of tillers/plant, panicle length, grain weight/panicle, and grain yield/plant, Karthikeyan *et al*. (2009) discovered that the ratio between the estimates of additive and dominance variances suggested a prevalence of non-additive gene action. Similar findings were reported by Singh *et al*. (2019) and Shikari *et al*. (2009). For days to 50% flowering, plant height, effective tillers/plant, panicle length, grains/panicle, 1000-grain weight, and grain yield/plant, Utharasu and Anandakumar (2013) discovered that dominance variance (σ^2D) was higher than additive variance (σ^2A) for most of the traits studied and Singh (2016) also observed higher dominance variance than additive variance for most of the traits studied.

Table 3. List of top specific combiners and general combiners for all the traits studied

Traits	Specific combiners	General combiners
Days to 50% flowering	HPR 2884 x HPR 2656 (12.57) HPR 2866 x HPR 2656 (12.13) HPR 2840 x HPR 1156 (8.38) HPR 2871 x HPR 2795 (5.49)	HPR 2889 (7.37) HPR 2843 (6.04) HPR 2871 (3.04) HPR 2870 (2.59)
Days to maturity	HPR 2840 x HPR 1156 (11.48) HPR 2884 x HPR 2656 (11.65) HPR 2866 x HPR 2656 (9.76) HPR 2643 x HPR 1156 (4.26)	HPR 2843 (5.65) HPR 2889 (5.21) HPR 2648 (3.44) HPR 2873 (3.32) HPR 1156 (0.52)
Plant height	HPR 2866 x HPR 1156 (9.98) HPR 2843 x HPR 2656 (9.92) HPR 2871 x HPR 2795 (9.42) HPR 2840 x HPR 2795 (8.85)	HPR 2840 (8.95) HPR 2884 (4.99) HPR 1156 (2.83)
Total tillers per plant	-	-
Panicle length	-	HPR 2840 (2.10)
Effective tillers per plant	HPR 2866 x HPR 1156 (2.31) HPR 2643 x HPR 2795 (2.09) HPR 2648 x HPR 2656 (1.91)	HPR 2648 (0.96) HPR 2871 (11.24)
L:B ratio	-	-
1000 seed wt.	HPR 2840 x HPR 2795 (4.99)	HPR 2884 (2.60)
Grain length	HPR 2866 x HPR 2795 (0.53) HPR 2889 x HPR 2795 (0.71) HPR 2870 x HPR 2795 (0.56)	HPR 2889 (0.41) HPR 2871 (0.44)
Grain breadth	HPR 2884 x HPR 2656 (0.21)	HPR 2873 (0.18)
Grains per panicle	HPR 2840 x HPR 2656 (23.82) HPR 2866 x HPR 1156 (26.83) HPR 2873 x HPR 2656 (19.25) HPR 2871 x HPR 2795 (15.99)	HPR 2840 (36.00) HPR 2866 (15.14) HPR 2887 (14.04) HPR 2884 (12.15)
Spikelets per panicle	HPR 2840 x HPR 2656 (40.76) HPR 2866 x HPR 1156 (28.50) HPR 2884 x HPR 2656 (27.14) HPR 2887 x HPR 1156 (19.81)	HPR 2840 (37.85) HPR 2884 (17.24)
Grain yield per plant	HPR 2866 x HPR 1156 (10.65) HPR 2877 x HPR 2795 (5.49) HPR 2648 x HPR 2656 (4.47) HPR 2887 x HPR 2795 (4.16)	HPR 2840 (10.84) HPR 2873 (6.224) HPR 2648 (3.159)

From the estimates of GCA and SCA for the genotypes, it was found that HPR 2889 is a good general combiner for days to 50% flowering, days to maturity, and grain length; HPR 2843 is a good general combiner for days to 50% flowering, days to maturity; HPR 2648 for days to maturity, effective tillers per plant and grain yield per plant; HPR 2840 for plant height, panicle length, grains per panicle, spikelets per panicle and grain yield per plant; HPR 2884 for plant height, 1000 seed weight, spikelets per panicle and grains per panicle; HPR 2871 for days to 50% flowering, effective tillers per plant and grain length and HPR 2873 for days to maturity, grain breadth and grain yield per plant.

There were some crosses that were found to be good specific combiners (Table 3) for various traits. HPR 2884 x HPR 2656 was a good specific combiner for days to 50 % flowering, days to maturity, spikelet fertility and grain breadth. HPR 2866 x HPR 2656 and HPR 2840 x HPR 1156 were good specific combiners for days to 50% flowering and days to maturity; HPR 2866 x HPR 1156 for plant height, effective tillers per plant, spikelets per panicle, grains per panicle and grain yield per plant; HPR 2871 x HPR 2795 for days to 50% flowering, plant height and grains per panicle; HPR 2840 x HPR 2656 for grains per panicle and spikelets per panicle.

The role of non-additive genes in the expression of yield and its components has already been investigated by Dalvi and Patel (2009), Saidaiah *et al.* (2010) and Selvaraj *et al.* (2011). SCA variances for grain quality measurements weregreater than GCA variances, according to Sreelakshmi and Babu (2017) and Thakare *et al.* (2010). The effects of GCA were investigated, and it was discovered that there were good general combiners for grain yield and other attributes among lines and testers. Significant SCA effects for diverse characters suggested a preponderance of non-additive gene actions in the inheritance of the characters under research, according to Akansha and Jaiswal (2019). Different lines and hybrids were discovered to be the best general and specific combiners for various yield and quality attributes. As a result, significant specific cross-combiners can be successfully used in crop improvement programmes to generate varieties, as well as additional confirmation of specific genes to develop gene-based ideal markers in rice breeding. Kargbo *et al.* (2019) also found similar results in their experiment in which they evaluated 27 hybrids along with their parents in L×T design. Kumar *et al.* (2019) and El- Mowafi *et al.* (2021) found in their experiments that both SCA and GCA were equally significant and both were responsible for expression of different traits. So, both additive and non-additive gene action equally contributed in governing various characters.

Hence these good general combiners of males and females may be used in future for hybrid rice breeding programme and the good specific combiners can be further tested for heterosis and utilized in heterosis breeding programs.

4. Conclusion

The present study indicated thatthe magnitude of dominance variance was much higher than additive variance for all the traits in the present material, except for total tillers per plant and grain yield per plant for which additive variance was quite higher in magnitude and the estimates of the average degree of dominance greater than 1, except for total tillers per plant also indicated that there was preponderance of dominant gene action or non-additive gene action in the expression of majority of the characters and their potential for use in exploitation of non-additive gene action for grain yield and other component traits by using genotypes in heterosis breeding and that the early selection will not be effective for these genotypes since most of the genotypes will segregate for many characters in future generations.On the basis of combining ability and gene action, the lines HPR 2840, HPR 2873, HPR 2889, crosses HPR 2840 x HPR 2656, HPR 2866 x HPR 1156, HPR 2871 x HPR 2795 were found to be promising for further improvement and utilization in breeding programmes.

Compliance with ethical standards

NA

Conflict of interest

No

Author contributions

PG and DPP: Conceptualization, Data curation, PG and DPP: Writing & updating the manuscript for publication, PG and DPP: Supervision, and Validation. All the listed authors read and approved the manuscript.

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